

## SEQUENCE LISTING

&lt;110&gt; HEGEMANN, Peter

<120> USE OF BIOLOGICAL PHOTORECEPTORS AS DIRECTLY LIGHT-CONTROLLED  
ION CHANNELS

&lt;130&gt; 231181

&lt;160&gt; 4

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 712

&lt;212&gt; PRT

&lt;213&gt; Chlamydomonas reinhardtii

&lt;220&gt;

<223> Amino acid sequence of CHOP-1 (AF461397) from  
Chlamydomonas reinhardtii

&lt;400&gt; 1

Met Ser Arg Arg Pro Trp Leu Leu Ala Leu Ala Leu Ala Val Ala Leu  
1 5 10 15Ala Ala Gly Ser Ala Gly Ala Ser Thr Gly Ser Asp Ala Thr Val Pro  
20 25 30Val Ala Thr Gln Asp Gly Pro Asp Tyr Val Phe His Arg Ala His Glu  
35 40 45Arg Met Leu Phe Gln Thr Ser Tyr Thr Leu Glu Asn Asn Gly Ser Val  
50 55 60Ile Cys Ile Pro Asn Asn Gly Gln Cys Phe Cys Leu Ala Trp Leu Lys  
65 70 75 80Ser Asn Gly Thr Asn Ala Glu Lys Leu Ala Ala Asn Ile Leu Gln Trp  
85 90 95Ile Thr Phe Ala Leu Ser Ala Leu Cys Leu Met Phe Tyr Gly Tyr Gln  
100 105 110Thr Trp Lys Ser Thr Cys Gly Trp Glu Glu Ile Tyr Val Ala Thr Ile  
115 120 125Glu Met Ile Lys Phe Ile Ile Glu Tyr Phe His Glu Phe Asp Glu Pro  
130 135 140Ala Val Ile Tyr Ser Ser Asn Gly Asn Lys Thr Val Trp Leu Arg Tyr  
145 150 155 160Ala Glu Trp Leu Leu Thr Cys Pro Val Ile Leu Ile His Leu Ser Asn  
165 170 175

Leu Thr Gly Leu Ala Asn Asp Tyr Asn Lys Arg Thr Met Gly Leu Leu  
 180 185 190  
 Val Ser Asp Ile Gly Thr Ile Val Trp Gly Thr Thr Ala Ala Leu Ser  
 195 200 205  
 Lys Gly Tyr Val Arg Val Ile Phe Phe Leu Met Gly Leu Cys Tyr Gly  
 210 215 220  
 Ile Tyr Thr Phe Phe Asn Ala Ala Lys Val Tyr Ile Glu Ala Tyr His  
 225 230 235 240  
 Thr Val Pro Lys Gly Ile Cys Arg Asp Leu Val Arg Tyr Leu Ala Trp  
 245 250 255  
 Leu Tyr Phe Cys Ser Trp Ala Met Phe Pro Val Leu Phe Leu Leu Gly  
 260 265 270  
 Pro Glu Gly Phe Gly His Ile Asn Gln Phe Asn Ser Ala Ile Ala His  
 275 280 285  
 Ala Ile Leu Asp Leu Ala Ser Lys Asn Ala Trp Ser Met Met Gly His  
 290 295 300  
 Phe Leu Arg Val Lys Ile His Glu His Ile Leu Leu Tyr Gly Asp Ile  
 305 310 315 320  
 Arg Lys Lys Gln Lys Val Asn Val Ala Gly Gln Glu Met Glu Val Glu  
 325 330 335  
 Thr Met Val His Glu Glu Asp Asp Glu Thr Gln Lys Val Pro Thr Ala  
 340 345 350  
 Lys Tyr Ala Asn Arg Asp Ser Phe Ile Ile Met Arg Asp Arg Leu Lys  
 355 360 365  
 Glu Lys Gly Phe Glu Thr Arg Ala Ser Leu Asp Gly Asp Pro Asn Gly  
 370 375 380  
 Asp Ala Glu Ala Asn Ala Ala Ala Gly Gly Lys Pro Gly Met Glu Met  
 385 390 395 400  
 Gly Lys Met Thr Gly Met Gly Met Gly Met Gly Ala Gly Met Gly Met  
 405 410 415  
 Ala Thr Ile Asp Ser Gly Arg Val Ile Leu Ala Val Pro Asp Ile Ser  
 420 425 430  
 Met Val Asp Phe Phe Arg Glu Gln Phe Ala Arg Leu Pro Val Pro Tyr  
 435 440 445  
 Glu Leu Val Pro Ala Leu Gly Ala Glu Asn Thr Leu Gln Leu Val Gln  
 450 455 460  
 Gln Ala Gln Ser Leu Gly Gly Cys Asp Phe Val Leu Met His Pro Glu

465		470		475		480									
Phe	Leu	Arg	Asp	Arg	Ser	Pro	Thr	Gly	Leu	Leu	Pro	Arg	Leu	Lys	Met
				485					490					495	
Gly	Gly	Gln	Arg	Ala	Ala	Ala	Phe	Gly	Trp	Ala	Ala	Ile	Gly	Pro	Met
			500					505					510		
Arg	Asp	Leu	Ile	Glu	Gly	Ser	Gly	Val	Asp	Gly	Trp	Leu	Glu	Gly	Pro
		515					520					525			
Ser	Phe	Gly	Ala	Gly	Ile	Asn	Gln	Gln	Ala	Leu	Val	Ala	Leu	Ile	Asn
	530					535					540				
Arg	Met	Gln	Gln	Ala	Lys	Lys	Met	Gly	Met	Met	Gly	Gly	Met	Gly	Met
545					550					555					560
Gly	Met	Gly	Gly	Gly	Met	Gly	Met	Gly	Met	Gly	Met	Gly	Met	Gly	Met
				565				570						575	
Ala	Pro	Ser	Met	Asn	Ala	Gly	Met	Thr	Gly	Gly	Met	Gly	Gly	Ala	Ser
			580					585						590	
Met	Gly	Gly	Ala	Val	Met	Gly	Met	Gly	Met	Gly	Met	Gln	Pro	Met	Gln
		595					600					605			
Gln	Ala	Met	Pro	Ala	Met	Ser	Pro	Met	Met	Thr	Gln	Gln	Pro	Ser	Met
610						615					620				
Met	Ser	Gln	Pro	Ser	Ala	Met	Ser	Ala	Gly	Gly	Ala	Met	Gln	Ala	Met
625					630					635					640
Gly	Gly	Val	Met	Pro	Ser	Pro	Ala	Pro	Gly	Gly	Arg	Val	Gly	Thr	Asn
				645					650					655	
Pro	Leu	Phe	Gly	Ser	Ala	Pro	Ser	Pro	Leu	Ser	Ser	Gln	Pro	Gly	Ile
			660					665					670		
Ser	Pro	Gly	Met	Ala	Thr	Pro	Pro	Ala	Ala	Thr	Ala	Ala	Pro	Ala	Ala
		675					680					685			
Gly	Gly	Ser	Glu	Ala	Glu	Met	Leu	Gln	Gln	Leu	Met	Ser	Glu	Ile	Asn
690						695					700				
Arg	Leu	Lys	Asn	Glu	Leu	Gly	Glu								
705					710										

&lt;210&gt; 2

&lt;211&gt; 737

&lt;212&gt; PRT

&lt;213&gt; Chlamydomonas reinhardtii

&lt;220&gt;

 <223> Amino acid sequence of CHOP-2 (AF461397) from  
 Chlamydomonas reinhardtii

&lt;400&gt; 2

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Met Asp Tyr Gly Gly Ala Leu Ser Ala Val Gly Arg Glu Leu Leu Phe
1      5      10      15
Val Thr Asn Pro Val Val Val Asn Gly Ser Val Leu Val Pro Glu Asp
20      25      30
Gln Cys Tyr Cys Ala Gly Trp Ile Glu Ser Arg Gly Thr Asn Gly Ala
35      40      45
Gln Thr Ala Ser Asn Val Leu Gln Trp Leu Ala Ala Gly Phe Ser Ile
50      55      60
Leu Leu Leu Met Phe Tyr Ala Tyr Gln Thr Trp Lys Ser Thr Cys Gly
65      70      75      80
Trp Glu Glu Ile Tyr Val Cys Ala Ile Glu Met Val Lys Val Ile Leu
85      90      95
Glu Phe Phe Phe Glu Phe Lys Asn Pro Ser Met Leu Tyr Leu Ala Thr
100     105     110
Gly His Arg Val Gln Trp Leu Arg Tyr Ala Glu Trp Leu Leu Thr Cys
115     120     125
Pro Val Ile Leu Ile His Leu Ser Asn Leu Thr Gly Leu Ser Asn Asp
130     135     140
Tyr Ser Arg Arg Thr Met Gly Leu Leu Val Ser Asp Ile Gly Thr Ile
145     150     155     160
Val Trp Gly Ala Thr Ser Ala Met Ala Thr Gly Tyr Val Lys Val Ile
165     170     175
Phe Phe Cys Leu Gly Leu Cys Tyr Gly Ala Asn Thr Phe Phe His Ala
180     185     190
Ala Lys Ala Tyr Ile Glu Gly Tyr His Thr Val Pro Lys Gly Arg Cys
195     200     205
Arg Gln Val Val Thr Gly Met Ala Trp Leu Phe Phe Val Ser Trp Gly
210     215     220
Met Phe Pro Ile Leu Phe Ile Leu Gly Pro Glu Gly Phe Gly Val Leu
225     230     235     240
Ser Val Tyr Gly Ser Thr Val Gly His Thr Ile Ile Asp Leu Met Ser
245     250     255
Lys Asn Cys Trp Gly Leu Leu Gly His Tyr Leu Arg Val Leu Ile His
260     265     270
Glu His Ile Leu Ile His Gly Asp Ile Arg Lys Thr Thr Lys Leu Asn
275     280     285

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Ile Gly Gly Thr Glu Ile Glu Val Glu Thr Leu Val Glu Asp Glu Ala  
 290 295 300  
 Glu Ala Gly Ala Val Asn Lys Gly Thr Gly Lys Tyr Ala Ser Arg Glu  
 305 310 315 320  
 Ser Phe Leu Val Met Arg Asp Lys Met Lys Glu Lys Gly Ile Asp Val  
 325 330 335  
 Arg Ala Ser Leu Asp Asn Ser Lys Glu Val Glu Gln Glu Gln Ala Ala  
 340 345 350  
 Arg Ala Ala Met Met Met Met Asn Gly Asn Gly Met Gly Met Gly Met  
 355 360 365  
 Gly Met Asn Gly Met Asn Gly Met Gly Gly Met Asn Gly Met Ala Gly  
 370 375 380  
 Gly Ala Lys Pro Gly Leu Glu Leu Thr Pro Gln Leu Gln Pro Gly Arg  
 385 390 395 400  
 Val Ile Leu Ala Val Pro Asp Ile Ser Met Val Asp Phe Phe Arg Glu  
 405 410 415  
 Gln Phe Ala Gln Leu Ser Val Thr Tyr Glu Leu Val Pro Ala Leu Gly  
 420 425 430  
 Ala Asp Asn Thr Leu Ala Leu Val Thr Gln Ala Gln Asn Leu Gly Gly  
 435 440 445  
 Val Asp Phe Val Leu Ile His Pro Glu Phe Leu Arg Asp Arg Ser Ser  
 450 455 460  
 Thr Ser Ile Leu Ser Arg Leu Arg Gly Ala Gly Gln Arg Val Ala Ala  
 465 470 475 480  
 Phe Gly Trp Ala Gln Leu Gly Pro Met Arg Asp Leu Ile Glu Ser Ala  
 485 490 495  
 Asn Leu Asp Gly Trp Leu Glu Gly Pro Ser Phe Gly Gln Gly Ile Leu  
 500 505 510  
 Pro Ala His Ile Val Ala Leu Val Ala Lys Met Gln Gln Met Arg Lys  
 515 520 525  
 Met Gln Gln Met Gln Gln Ile Gly Met Met Thr Gly Gly Met Asn Gly  
 530 535 540  
 Met Gly Gly Gly Met Gly Gly Gly Met Asn Gly Met Gly Gly Gly Asn  
 545 550 555 560  
 Gly Met Asn Asn Met Gly Asn Gly Met Gly Gly Gly Met Gly Asn Gly  
 565 570 575  
 Met Gly Gly Asn Gly Met Asn Gly Met Gly Gly Gly Asn Gly Met Asn  
 580 585 590

Asn Met Gly Gly Asn Gly Met Ala Gly Asn Gly Met Gly Gly Gly Met  
 595 600 605  
 Gly Gly Asn Gly Met Gly Gly Ser Met Asn Gly Met Ser Ser Gly Val  
 610 615 620  
 Val Ala Asn Val Thr Pro Ser Ala Ala Gly Gly Met Gly Gly Met Met  
 625 630 635 640  
 Asn Gly Gly Met Ala Ala Pro Gln Ser Pro Gly Met Asn Gly Gly Arg  
 645 650 655  
 Leu Gly Thr Asn Pro Leu Phe Asn Ala Ala Pro Ser Pro Leu Ser Ser  
 660 665 670  
 Gln Leu Gly Ala Glu Ala Gly Met Gly Ser Met Gly Gly Met Gly Gly  
 675 680 685  
 Met Ser Gly Met Gly Gly Met Gly Gly Met Gly Gly Met Gly Gly Ala  
 690 695 700  
 Gly Ala Ala Thr Thr Gln Ala Ala Gly Gly Asn Ala Glu Ala Glu Met  
 705 710 715 720  
 Leu Gln Asn Leu Met Asn Glu Ile Asn Arg Leu Lys Arg Glu Leu Gly  
 725 730 735

Glu

<210> 3

<211> 259

<212> PRT

<213> Halobacterium salinarum

<220>

<223> Amino acid sequence of bacteriorhodopsin from  
Halobacterium salinarum

<400> 3

Met Leu Pro Thr Ala Val Glu Gly Val Ser Gln Ala Gln Ile Thr Gly  
 1 5 10 15

Arg Pro Glu Trp Ile Trp Leu Ala Leu Gly Thr Ala Leu Met Gly Leu  
 20 25 30

Gly Thr Leu Tyr Phe Leu Val Lys Gly Met Gly Val Ser Asp Pro Asp  
 35 40 45

Ala Lys Lys Phe Tyr Ala Ile Thr Thr Leu Val Pro Ala Ile Ala Phe  
 50 55 60

Thr Met Tyr Leu Ser Met Leu Leu Gly Tyr Gly Leu Thr Met Val Pro  
 65 70 75 80

Phe Gly Gly Glu Gln Asn Pro Ile Tyr Trp Ala Arg Tyr Ala Asp Trp

85										90					95				
Leu	Phe	Thr	Thr	Pro	Leu	Leu	Leu	Leu	Asp	Leu	Ala	Leu	Leu	Val	Asp				
			100						105					110					
Ala	Asp	Gln	Gly	Thr	Ile	Leu	Ala	Leu	Val	Gly	Ala	Asp	Gly	Ile	Met				
		115					120					125							
Ile	Gly	Thr	Gly	Leu	Val	Gly	Ala	Leu	Thr	Lys	Val	Tyr	Ser	Tyr	Arg				
	130					135					140								
Phe	Val	Trp	Trp	Ala	Ile	Ser	Thr	Ala	Ala	Met	Leu	Tyr	Ile	Leu	Tyr				
145					150					155					160				
Val	Leu	Phe	Phe	Gly	Phe	Thr	Ser	Lys	Ala	Glu	Ser	Met	Arg	Pro	Glu				
				165					170					175					
Val	Ala	Ser	Thr	Phe	Lys	Val	Leu	Arg	Asn	Val	Thr	Val	Val	Leu	Trp				
			180					185						190					
Ser	Ala	Tyr	Pro	Val	Val	Trp	Leu	Ile	Gly	Ser	Glu	Gly	Ala	Gly	Ile				
		195					200					205							
Val	Pro	Leu	Asn	Ile	Glu	Thr	Leu	Leu	Phe	Met	Val	Leu	Asp	Val	Ser				
	210					215					220								
Ala	Lys	Val	Gly	Phe	Gly	Leu	Ile	Leu	Leu	Arg	Ser	Arg	Ala	Ile	Phe				
225					230					235					240				
Gly	Glu	Ala	Glu	Ala	Pro	Glu	Pro	Ser	Ala	Gly	Asp	Gly	Ala	Ala	Ala				
				245					250					255					
Thr Ser Asp																			

&lt;210&gt; 4

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Chlamydomonas reinhardtii

&lt;220&gt;

&lt;223&gt; Amino acid sequence of the CHOP2-315/H134R mutant

&lt;400&gt; 4

Met	Asp	Tyr	Gly	Gly	Ala	Leu	Ser	Ala	Val	Gly	Arg	Glu	Leu	Leu	Phe
1				5					10					15	

Val	Thr	Asn	Pro	Val	Val	Val	Asn	Gly	Ser	Val	Leu	Val	Pro	Glu	Asp
			20					25					30		

Gln	Cys	Tyr	Cys	Ala	Gly	Trp	Ile	Glu	Ser	Arg	Gly	Thr	Asn	Gly	Ala
	35						40					45			

Gln Thr Ala Ser Asn Val Leu Gln Trp Leu Ala Ala Gly Phe Ser Ile  
 50 55 60  
 Leu Leu Leu Met Phe Tyr Ala Tyr Gln Thr Trp Lys Ser Thr Cys Gly  
 65 70 75 80  
 Trp Glu Glu Ile Tyr Val Cys Ala Ile Glu Met Val Lys Val Ile Leu  
 85 90 95  
 Glu Phe Phe Phe Glu Phe Lys Asn Pro Ser Met Leu Tyr Leu Ala Thr  
 100 105 110  
 Gly His Arg Val Gln Trp Leu Arg Tyr Ala Glu Trp Leu Leu Thr Cys  
 115 120 125  
 Pro Val Ile Leu Ile Arg Leu Ser Asn Leu Thr Gly Leu Ser Asn Asp  
 130 135 140  
 Tyr Ser Arg Arg Thr Met Gly Leu Leu Val Ser Asp Ile Gly Thr Ile  
 145 150 155 160  
 Val Trp Gly Ala Thr Ser Ala Met Ala Thr Gly Tyr Val Lys Val Ile  
 165 170 175  
 Phe Phe Cys Leu Gly Leu Cys Tyr Gly Ala Asn Thr Phe Phe His Ala  
 180 185 190  
 Ala Lys Ala Tyr Ile Glu Gly Tyr His Thr Val Pro Lys Gly Arg Cys  
 195 200 205  
 Arg Gln Val Val Thr Gly Met Ala Trp Leu Phe Phe Val Ser Trp Gly  
 210 215 220  
 Met Phe Pro Ile Leu Phe Ile Leu Gly Pro Glu Gly Phe Gly Val Leu  
 225 230 235 240  
 Ser Val Tyr Gly Ser Thr Val Gly His Thr Ile Ile Asp Leu Met Ser  
 245 250 255  
 Lys Asn Cys Trp Gly Leu Leu Gly His Tyr Leu Arg Val Leu Ile His  
 260 265 270



Glu His Ile Leu Ile His Gly Asp Ile Arg Lys Thr Thr Lys Leu Asn  
 275 280 285

Ile Gly Gly Thr Glu Ile Glu Val Glu Thr Leu Val Glu Asp Glu Ala  
 290 295 300

Glu Ala Gly Ala Val Asn Lys Gly Thr Gly Lys  
 305 310 315